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#25

SEQUENCE LISTING

<110> Brugliera, Filippa
Holton, Timothy A.
Michael, Michael Z.

<120> GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
AND USES THEREFOR

<130> 11658

<140> 09/142,108
<141> 1998-09-01

<150> PN8386
<151> 1996-03-01

<160> 45

<170> PatentIn Ver. 2.1

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Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His Leu Gly Pro
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Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala Ala Ser Ala
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Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp Phe Arg His			
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Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu Ala Ser Ala			
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Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr Thr			
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Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser Met Val Val			
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His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly			
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1789

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<213> Petunia x hybrida

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35 40 45
Leu Gly Pro Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr
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Gly Pro Leu Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala
65 70 75 80
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85 90 95
Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn
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115 120 125
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130 135 140
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165 170 175
Cys Thr Thr Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe
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195 200 205
Met Val Val Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp
210 215 220
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225 230 235 240
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260 265 270
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275 280 285
Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala
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Gly Thr Asp Thr Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu
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Val Val Gly Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu
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 Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala
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 450 455 460
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 Asn Leu Tyr Tyr Leu Ile Thr Thr Val Phe Arg Gly His Gln Lys Pro
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 Leu Pro Pro Gly Pro Arg Pro Trp Pro Ile Val Gly Asn Leu Pro His
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 Met Gly Gln Ala Pro His Gln Gly Leu Ala Ala Leu Ala Gln Lys Tyr
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Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg Met Leu			
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Arg Lys Ile Cys Ser Leu His Met Phe Ser Ser Lys Ala Leu Asp Asp			
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Phe Arg Leu Val Arg Gln Glu Val Ser Ile Leu Val Asn Ala Ile			
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Phe Val Pro Ala Leu Glu Cys Leu Asp Leu Gln Gly Val Ala Ser Lys			
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375	380	385	
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420	425	430	
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455	460	465	
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470	475	480	
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35 40 45
Lys Tyr Gly Pro Leu Leu Tyr Met Arg Leu Gly Tyr Val Asp Val Val
50 55 60
Val Ala Ala Ser Ala Ser Val Ala Thr Gln Phe Leu Lys Thr His Asp
65 70 75 80
Leu Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His Ile Ala
85 90 95
Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg
100 105 110
Met Leu Arg Lys Ile Cys Ser Leu His Met Phe Ser Ser Lys Ala Leu
115 120 125
Asp Asp Phe Arg Leu Val Arg Gln Glu Glu Val Ser Ile Leu Val Asn
130 135 140
Ala Ile Ala Lys Ala Gly Thr Lys Pro Val Gln Leu Gly Gln Leu Leu
145 150 155 160
Asn Val Cys Thr Thr Asn Ala Leu Ser Arg Val Met Leu Gly Lys Arg
165 170 175
Val Leu Gly Asp Gly Thr Gly Lys Ser Asp Pro Lys Ala Glu Glu Phe
180 185 190
Lys Asp Met Val Leu Glu Leu Met Val Leu Thr Gly Val Phe Asn Ile
195 200 205
Gly Asp Phe Val Pro Ala Leu Glu Cys Leu Asp Leu Gln Gly Val Ala
210 215 220
Ser Lys Met Lys Lys Leu His Lys Arg Leu Asp Asn Phe Met Ser Asn
225 230 235 240
Ile Leu Glu Glu His Lys Ser Val Ala His Gln Gln Asn Gly Asp
245 250 255
Leu Leu Ser Ile Leu Ile Ser Leu Lys Asp Asn Cys Asp Gly Glu Gly
260 265 270
Gly Lys Phe Ser Ala Thr Glu Ile Lys Ala Leu Leu Leu Asp Leu Phe
275 280 285
Thr Ala Gly Thr Asp Thr Ser Ser Ser Thr Thr Glu Trp Ala Ile Ala
290 295 300
Glu Leu Ile Arg His Pro Lys Ile Leu Ala Gln Val Gln Gln Glu Met
305 310 315 320
Asp Ser Val Val Gly Arg Asp Arg Leu Ile Ala Glu Ala Asp Ile Pro
325 330 335
Asn Leu Thr Tyr Phe Gln Ala Val Ile Lys Glu Val Phe Arg Leu His
340 345 350
Pro Ser Thr Pro Leu Ser Leu Pro Arg Val Ala Asn Glu Ser Cys Glu
355 360 365
Ile Asn Gly Tyr His Ile Pro Lys Asn Thr Thr Leu Leu Val Asn Val
370 375 380
Trp Ala Ile Ala Arg Asp Pro Glu Val Trp Ala Asp Pro Leu Glu Phe
385 390 395 400
Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val Asp Val
405 410 415
Lys Gly Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile

420	425	430
Cys Ala Gly Leu Ser Leu Gly Leu Arg Met Val Gln Leu Met Thr Ala		
435	440	445
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450	455	460
Glu Lys Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln Arg Lys		
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10 15 20

ttt ata tta ggg ttc ttg ctt cta tat tcc ttc ctc aac aaa aaa gta 210
Phe Ile Leu Gly Phe Leu Leu Tyr Ser Phe Leu Asn Lys Lys Val
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aag cca ctg cca cct gga ccg aag cca tgg ccc atc gtc gga aat ctg 258
Lys Pro Leu Pro Gly Pro Lys Pro Trp Pro Ile Val Gly Asn Leu
45 50 55

cca cat ctt ggg ccg aag ccc cac cag tcg atg gcg gcg ctg gca cg 306
Pro His Leu Gly Pro Lys Pro His Gln Ser Met Ala Ala Leu Ala Arg
60 65 70

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Val His Gly Pro Leu Ile His Leu Lys Met Gly Phe Val His Val Val
75 80 85

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90 95 100

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105 110 115 120

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Val Val Gly His Ala Asp Ser Lys Ala Glu Glu Phe Lys Ala Met Val			
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Val Glu Leu Met Val Leu Ala Gly Val Phe Asn Leu Gly Asp Phe Ile			
220	225	230	
cca cct ctt gaa aaa ttg gat ctt caa ggt gtc att gct aag atg aag		834	
Pro Pro Leu Glu Lys Leu Asp Leu Gln Gly Val Ile Ala Lys Met Lys			
235	240	245	
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Lys Leu His Leu Arg Phe Asp Ser Phe Leu Ser Lys Ile Leu Gly Asp			
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aac atg tta att tct ttg aag gac gct gat gat gcc gaa gga ggg agg		978	
Asn Met Leu Ile Ser Leu Lys Asp Ala Asp Asp Ala Glu Gly Gly Arg			
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Leu Thr Asp Val Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Ala Ala			
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gga act gac aca aca tca agc act gtg gaa tgg tgc ata gct gag tta		1074	
Gly Thr Asp Thr Thr Ser Ser Thr Val Glu Trp Cys Ile Ala Glu Leu			
315	320	325	
gta cga cat cct gaa atc ctt gcc caa gtc caa aaa gaa ctc gac tct		1122	
Val Arg His Pro Glu Ile Leu Ala Gln Val Gln Lys Glu Leu Asp Ser			
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Val Val Gly Lys Asn Arg Val Val Lys Glu Ala Asp Leu Ala Gly Leu				
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cca ttc ctc caa gcg gtc gtc aag gaa aat ttc cga ctc cat ccc tcc				1218
Pro Phe Leu Gln Ala Val Val Lys Glu Asn Phe Arg Leu His Pro Ser				
365	370	375		
acc ccg ctc tcc cta ccg agg atc gca cat gag agt tgt gaa gtg aat				1266
Thr Pro Leu Ser Leu Pro Arg Ile Ala His Glu Ser Cys Glu Val Asn				
380	385	390		
gga tac ttg att cca aag ggt tcg aca ctt ctt gtc aat gtt tgg gca				1314
Gly Tyr Leu Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala				
395	400	405		
att gct cgc gat cca aat gtg tgg gat gaa cca cta gag ttc cgg cct				1362
Ile Ala Arg Asp Pro Asn Val Trp Asp Glu Pro Leu Glu Phe Arg Pro				
410	415	420		
gaa cga ttc ttg aag ggc ggg gaa aag cct aat gtc gat gtt aga ggg				1410
Glu Arg Phe Leu Lys Gly Glu Lys Pro Asn Val Asp Val Arg Gly				
425	430	435	440	
aat gat ttc gaa ttg ata ccg ttc gga gcg ggc cga aga att tgt gca				1458
Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala				
445	450	455		
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Gly Met Ser Leu Gly Ile Arg Met Val Gln Leu Leu Thr Ala Thr Leu				
460	465	470		
aac cat gcg ttt gac ttt gat ttg gcg gat gga cag ttg cct gaa agc				1554
Asn His Ala Phe Asp Phe Asp Leu Ala Asp Gly Gln Leu Pro Glu Ser				
475	480	485		
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Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro				
490	495	500		
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Pro Trp Pro Ile Val Gly Asn Leu Pro His	Leu Gly Pro Lys Pro His	
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Gln Ser Met Ala Ala Leu Ala Arg Val His	Gly Pro Leu Ile His Leu	
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Lys Met Gly Phe Val His Val Val Ala Ser	Ser Ala Ser Val Ala	
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Glu Lys Phe Leu Lys Val His Asp Ala Asn Phe	Ser Ser Arg Pro Pro	
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Asn Ser Gly Ala Lys His Val Ala Tyr Asn	Tyr Gln Asp Leu Val Phe	
115	120	125
Ala Pro Tyr Gly Pro Arg Trp Arg Met	Leu Arg Lys Ile Cys Ala Leu	
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His Leu Phe Ser Ala Lys Ala Leu Asn Asp	Phe Thr His Val Arg Gln	
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Asp Glu Val Gly Ile Leu Thr Arg Val	Leu Ala Asp Ala Gly Glu	Thr
165	170	175
Pro Leu Lys Leu Gly Gln Met Met Asn Thr	Cys Ala Thr Asn Ala Ile	
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Ala Arg Val Met Leu Gly Arg Arg Val Val	Gly His Ala Asp Ser Lys	
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Ala Glu Glu Phe Lys Ala Met Val Val	Glu Leu Met Val Leu Ala Gly	
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Val Phe Asn Leu Gly Asp Phe Ile Pro Pro	Leu Glu Lys Leu Asp Leu	
225	230	235
Gln Gly Val Ile Ala Lys Met Lys Lys	Leu His Leu Arg Phe Asp Ser	
245	250	255
Phe Leu Ser Lys Ile Leu Gly Asp His Lys	Ile Asn Ser Ser Asp Glu	
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Thr Lys Gly His Ser Asp Leu Leu Asn Met	Leu Ile Ser Leu Lys Asp	
275	280	285
Ala Asp Asp Ala Glu Gly Gly Arg Leu Thr	Asp Val Glu Ile Lys Ala	
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Val Glu Trp Cys Ile Ala Glu Leu Val Arg	His Pro Glu Ile Leu Ala	
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Gln Val Gln Lys Glu Leu Asp Ser Val Val	Gly Lys Asn Arg Val Val	
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Lys Glu Ala Asp Leu Ala Gly Leu Pro Phe	Leu Gln Ala Val Val Lys	
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Glu Asn Phe Arg Leu His Pro Ser Thr Pro	Leu Ser Leu Pro Arg Ile	
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Ala His Glu Ser Cys Glu Val Asn Gly Tyr	Leu Ile Pro Lys Gly Ser	
385	390	395
Thr Leu Leu Val Asn Val Trp Ala Ile Ala	Arg Asp Pro Asn Val Trp	
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Asp Glu Pro Leu Glu Phe Arg Pro Glu Arg	Phe Leu Lys Gly Gly Glu	
420	425	430
Lys Pro Asn Val Asp Val Arg Gly Asn Asp	Phe Glu Leu Ile Pro Phe	
435	440	445
Gly Ala Gly Arg Arg Ile Cys Ala Gly Met	Ser Leu Gly Ile Arg Met	
450	455	460
Val Gln Leu Leu Thr Ala Thr Leu Asn His	Ala Phe Asp Phe Asp Leu	
465	470	475
Ala Asp Gly Gln Leu Pro Glu Ser Leu Asn Met	Glu Glu Ala Tyr Gly	

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165

170

175

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 Leu His Ala Asn Val Ala His Lys His Leu Ile Gly Asn Phe Ser Trp
 195 200 205

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 50 55 60
Glu Leu Asp Ile Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser Asp
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 85 90 95
Leu His Pro Pro Thr Pro Leu Ser Leu Pro His Ile Ala Ser Glu Ser
 100 105 110
Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Phe Asp
 115 120 125

Gly His Met Gly Leu Gly Arg Asp Pro Asp Gln Trp Ser Asp Pro Leu
 130 135 140

Ala Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Ser Gly Val
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 Asp Val Lys Gly Ser Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg
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 Pro Ile Cys Ala Gly Leu Ser Leu Gly Leu Arg Thr Asp Leu Ser Cys
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 Arg Ser Tyr Ala Gly Gln Pro Glu Tyr Arg Arg Lys Ser Leu Leu Gly
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 Phe Thr Leu Gln Arg Ala Val Pro Ser Val Val His Pro Lys Pro Arg
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Ala Gly Val Phe Asn Ile Gly Asp Phe Val Pro Ser Leu Asp Trp Leu	
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Asp Ala Phe Leu Ser Ser Ile Leu Lys Glu His Glu Met Asn Gly Gln				
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Thr Asp Leu Asp Gly Asp Gly Ser Leu Thr Asp Thr Glu Ile Lys				
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tctagt gcta	ggtacgg ctc	ttt gttc	tacacat	ttt	ttttaat	ggctt atct	5537				
agaactt tga	aggat accat	ttt atttt	ttggacaa	ag	aaggat	atcc	5597				
acactttaat	gttggattaa	ctaacttatt	atgc	cattt	aatggc	cctac	5657				
gacacaagct	tgattt gg	ttt	ataaaaaa	ag	tgcactataa	tctt	tttta	ctgaa	ccctt	5717	
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caaccgaaag	cagtggattt	gcgc	tctt	actcc	acaa	c	tttgc	tta	accgg	ctt	6377
gttctctcgt	gatgatgctc	tga	agaagaa	tcacc	gtt	c	tttgc	tta	atgctt	atgc	6437
aaaaaaaaat	gttatttata	tgtt	cttgc	tttgc	gtt	tttgc	tttgc	tttgc	tttgc	tttgc	6497
ttcttttta	cttccgg	ttt	caagaa	aaac	aattat	caat	gt	aaaac	ccaa	atctactat	6557
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 Ile Leu Arg Ile Phe Ser His Arg Arg Asn Arg Ser His Asn Asn Arg
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 Leu Pro Pro Gly Pro Asn Pro Trp Pro Ile Ile Gly Asn Leu Pro His
 35 40 45
 Met Gly Thr Lys Pro His Arg Thr Leu Ser Ala Met Val Thr Thr Tyr
 50 55 60
 Gly Pro Ile Leu His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala
 65 70 75 80
 Ala Ser Lys Ser Val Ala Glu Gln Phe Leu Lys Ile His Asp Ala Asn
 85 90 95
 Phe Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Met Ala Tyr Asn
 100 105 110
 Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly His Arg Trp Arg Leu Leu
 115 120 125
 Arg Lys Ile Ser Ser Val His Leu Phe Ser Ala Lys Ala Leu Glu Asp
 130 135 140
 Phe Lys His Val Arg Gln
 145 150

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 Gly Arg Glu Met Ile Gly Arg Arg Leu Phe Gly Ala Asp Ala Asp His
 35 40 45
 Lys Ala Asp Glu Phe Arg Ser Met Val Thr Glu Met Met Ala Leu Ala
 50 55 60
 Gly Val Phe Asn Ile Gly Asp Phe Val Pro Ser Leu Asp Trp Leu Asp
 65 70 75 80

Leu Gln Gly Val Ala Gly Lys Met Lys Arg Leu His Lys Arg Phe Asp
 85 90 95
 Ala Phe Leu Ser Ser Ile Leu Lys Glu His Glu Met Asn Gly Gln Asp

100

105

110

Gln Lys His Thr Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly Thr
115 120 125

Asp Leu Asp Gly Asp Gly Gly Ser Leu Thr Asp Thr Glu Ile Lys Ala
130 135 140

Leu Leu Leu
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35 40 45

Asp Ile Ala Gln Leu Pro Tyr Leu Gln
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<211> 159
<212> PRT
<213> Arabidopsis thaliana

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20 25 30

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35 40 45

Pro Asp Gln Trp Ser Asp Pro Leu Ala Phe Lys Pro Glu Arg Phe Leu
50 55 60

Pro Gly Gly Glu Lys Ser Gly Val Asp Val Lys Gly Ser Asp Phe Glu
65 70 75 80

Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Leu
85 90 95

Gly Leu Arg Thr Ile Gln Phe Leu Thr Ala Thr Leu Val Gln Gly Phe
100 105 110

Asp Trp Glu Leu Ala Gly Gly Val Thr Pro Glu Lys Leu Asn Met Glu
115 120 125

Glu Ser Tyr Gly Leu Thr Leu Gln Arg Ala Val Pro Leu Val Val His
130 135 140

Pro Lys Pro Arg Leu Ala Pro Asn Val Tyr Gly Leu Gly Ser Gly
145 150 155

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<211> 1748

<212> DNA

<213> Rosa hybrida

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<221> CDS

<222> (22)..(1563)

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Phe Ala Val Phe Arg Leu Leu Phe Ser Gly Lys Ser Gln Arg
15 20 25

cac tcg ctc cct ctc cct ggc ccc aaa cca tgg ccg gtg gtt ggc 147
His Ser Ile Pro Leu Pro Pro Gly Pro Lys Pro Trp Pro Val Val Gly
30 35 40

aac tta cct cac ttg ggc ccc ttc ccg cac cac tcc atc gcg gag ttg 195
Asn Leu Pro His Leu Gly Pro Phe Pro His His Ser Ile Ala Glu Leu
45 50 55

gcg aag aaa cac ggg ccg ctc atg cac ctc cgc ctc ggc tac gtt gac 243
Ala Lys Lys His Gly Pro Leu Met His Leu Arg Leu Gly Tyr Val Asp
60 65 70

gta gtc gtg gcg gca tca gca tcc gta gcg gcc cag ttc ttg aag act 291

Val Val Val Ala Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr
75 80 85 90

cac gac gcc aat ttc tcc agc cga ccg ccc aac tcc ggc gcc aag cac 339
His Asp Ala Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His
95 100 105

ctc gcc tat aac tac cag gac ctc gtg ttc agg ccg tac ggt cca cg 387
Leu Ala Tyr Asn Tyr Gln Asp Leu Val Phe Arg Pro Tyr Gly Pro Arg
110 115 120

tgg cgc atg ttc cgg aag atc agc tcc gtc cat ctg ttc tcc ggc aaa 435
Trp Arg Met Phe Arg Lys Ile Ser Ser Val His Leu Phe Ser Gly Lys
125 130 135

gcc ttg gat gat ctt aaa cac gtc cg ^g cag gag gag gta agt gtg cta Ala Leu Asp Asp Leu Lys His Val Arg Gln Glu Glu Val Ser Val Leu 140 145 150	483
gcg cat gcc ttg gca aat tca ggg tca aag gta gtg aac ctg gc ^g caa Ala His Ala Leu Ala Asn Ser Gly Ser Lys Val Val Asn Leu Ala Gln 155 160 165 170	531
ctg ctg aac ctg tgc acg gtc aat gct cta gga agg gtg atg gta ggg Leu Leu Asn Leu Cys Thr Val Asn Ala Leu Gly Arg Val Met Val Gly 175 180 185	579
cg ^g agg gtt ttc ggc gac ggc agc gga ggc gac gat ccg aag gc ^g gac Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Asp Asp Pro Lys Ala Asp 190 195 200	627
gag ttc aaa tcg atg gtg gtg qag atg atg qtg ttg qca gga gtg ttc Glu Phe Lys Ser Met Val Val Glu Met Met Val Leu Ala Gly Val Phe 205 210 215	675
aac ata ggt gac ttc atc ccc tct ctc gaa tgg ctt gac ttg caa gg ^c Asn Ile Gly Asp Phe Ile Pro Ser Leu Glu Trp Leu Asp Leu Gln Gly 220 225 230	723
gtg gc ^g tcc aag atg aag aag ctc cac aag aga tt ^c gac gac tt ^c Val Ala Ser Lys Met Lys Lys Leu His Lys Arg Phe Asp Asp Phe Leu 235 240 245 250	771
aca gcc att gtc gag gac cac aag aag gg ^c tcc ggc acg gc ^g ggg cac Thr Ala Ile Val Glu Asp His Lys Lys Gly Ser Gly Thr Ala Gly His 255 260 265	819
gtc gac atg ttg acc act ctg ctc tcg ctc aag gaa gac gg ^c gac gg ^c Val Asp Met Leu Thr Thr Leu Leu Ser Leu Lys Glu Asp Ala Asp Gly 270 275 280	867
gaa gga gg ^c aag ctc acc gat act gaa atc aaa gct ttg ctt ttg aac Glu Gly Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn 285 290 295	915
atg ttc acg gct gg ^c act gat acg tca tcg agc acg gtg gaa tgg gca Met Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp Ala 300 305 310	963
ata gct gaa ctc att cg ^g cac cct cat atg cta gc ^g cga gtt cag aaa Ile Ala Glu Leu Ile Arg His Pro His Met Leu Ala Arg Val Gln Lys 315 320 325 330	1011
gag ctt gac gat tt ^t gtt gg ^c cat gac cga ctt gtg acc gaa tcc gac Glu Leu Asp Asp Phe Val Gly His Asp Arg Leu Val Thr Glu Ser Asp 335 340 345	1059
ata ccc aac ctc cct tac ctc caa gg ^c gtg atc aag gaa acg tt ^c cga Ile Pro Asn Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Thr Phe Arg 350 355 360	1107
ctc cac cca tcc act cct ctc tcg tt ^t cct cgt atg gca gg ^c gag agt Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Ala Ala Glu Ser 365 370 375	1155

tgc gaa atc aac ggg tac cac atc ccg aaa ggc tcc aca ctc ttg gtc Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Leu Val 380 385 390	1203
aat gta tgg gcc ata tcg cgt gac ccg gct gaa tgg gcc gac cca ctg Asn Val Trp Ala Ile Ser Arg Asp Pro Ala Glu Trp Ala Asp Pro Leu 395 400 405 410	1251
gag ttc aag ccc gag agg ttc ctg ccg ggg ggc gaa aag cct aat gtt Glu Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val 415 420 425	1299
gat att aga gga aac gat ttt gaa gtc ata ccc ttc ggt gcc ggg cga Asp Ile Arg Gly Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg 430 435 440	1347
aga ata tgt gcc ggg atg agc ttg ggc ctg cgt atg gtc cat tta atg Arg Ile Cys Ala Gly Met Ser Leu Gly Leu Arg Met Val His Leu Met 445 450 455	1395
act gca aca ttg gtc cac gca ttt aat tgg gcc ttg gct gat ggg ctg Thr Ala Thr Leu Val His Ala Phe Asn Trp Ala Leu Ala Asp Gly Leu 460 465 470	1443
acc gct gag aag tta aac atg gat gaa gca tat ggg ctc act cta caa Thr Ala Glu Lys Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln 475 480 485 490	1491
cga gct gca ccg tta atg gtg cac ccg cgc acc agg ctg gcc cca cag Arg Ala Ala Pro Leu Met Val His Pro Arg Thr Arg Leu Ala Pro Gln 495 500 505	1539
gca tat aaa act tca tca tct taa ttagagagct atgttctggg tggcccggt 1593	
Ala Tyr Lys Thr Ser Ser Ser 510	
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taatttatga atacttatga tataggcgac agcaa 1748	

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<211> 513
<212> PRT
<213> Rosa hybrida

<400> 15

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Pro Gly Pro Lys Pro Trp Pro Val Val Gly Asn Leu Pro His Leu Gly 35 40 45
Pro Phe Pro His His Ser Ile Ala Glu Leu Ala Lys Lys His Gly Pro 50 55 60
Leu Met His Leu Arg Leu Gly Tyr Val Asp Val Val Ala Ala Ser

65	70	75	80
Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn Phe Ser			
85	90	95	
Ser Arg Pro Pro Asn Ser Gly Ala Lys His Leu Ala Tyr Asn Tyr Gln			
100	105	110	
Asp Leu Val Phe Arg Pro Tyr Gly Pro Arg Trp Arg Met Phe Arg Lys			
115	120	125	
Ile Ser Ser Val His Leu Phe Ser Gly Lys Ala Leu Asp Asp Leu Lys			
130	135	140	
His Val Arg Gln Glu Glu Val Ser Val Leu Ala His Ala Leu Ala Asn			
145	150	155	160
Ser Gly Ser Lys Val Val Asn Leu Ala Gln Leu Leu Asn Leu Cys Thr			
165	170	175	
Val Asn Ala Leu Gly Arg Val Met Val Gly Arg Arg Val Phe Gly Asp			
180	185	190	
Gly Ser Gly Gly Asp Asp Pro Lys Ala Asp Glu Phe Lys Ser Met Val			
195	200	205	
Val Glu Met Met Val Leu Ala Gly Val Phe Asn Ile Gly Asp Phe Ile			
210	215	220	
Pro Ser Leu Glu Trp Leu Asp Leu Gln Gly Val Ala Ser Lys Met Lys			
225	230	235	240
Lys Leu His Lys Arg Phe Asp Asp Phe Leu Thr Ala Ile Val Glu Asp			
245	250	255	
His Lys Lys Gly Ser Gly Thr Ala Gly His Val Asp Met Leu Thr Thr			
260	265	270	
Leu Leu Ser Leu Lys Glu Asp Ala Asp Gly Glu Gly Lys Leu Thr			
275	280	285	
Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Met Phe Thr Ala Gly Thr			
290	295	300	
Asp Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg			
305	310	315	320
His Pro His Met Leu Ala Arg Val Gln Lys Glu Leu Asp Asp Phe Val			
325	330	335	
Gly His Asp Arg Leu Val Thr Glu Ser Asp Ile Pro Asn Leu Pro Tyr			
340	345	350	
Leu Gln Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro			
355	360	365	
Leu Ser Leu Pro Arg Met Ala Ala Glu Ser Cys Glu Ile Asn Gly Tyr			
370	375	380	
His Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ser			
385	390	395	400
Arg Asp Pro Ala Glu Trp Ala Asp Pro Leu Glu Phe Lys Pro Glu Arg			
405	410	415	
Phe Leu Pro Gly Gly Glu Lys Pro Asn Val Asp Ile Arg Gly Asn Asp			
420	425	430	
Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met			
435	440	445	
Ser Leu Gly Leu Arg Met Val His Leu Met Thr Ala Thr Leu Val His			
450	455	460	
Ala Phe Asn Trp Ala Leu Ala Asp Gly Leu Thr Ala Glu Lys Leu Asn			
465	470	475	480
Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met			
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Val His Pro Arg Thr Arg Leu Ala Pro Gln Ala Tyr Lys Thr Ser Ser			
500	505	510	
Ser			

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<212> DNA
<213> Chrysanthemum

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<221> CDS
<222> (4)..(1530)

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gta ctc tat gta ttt ctt aac tta agt tca cgt aaa tcc gcc aga ctc 96
Val Leu Tyr Val Phe Leu Asn Leu Ser Ser Arg Lys Ser Ala Arg Leu
20 25 30

cca ccc ggg cca aca cca tgg cct ata gtc ggg aac tta cca cac ctt 144
Pro Pro Gly Pro Thr Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu
35 40 45

ggc cca atc cca cac cac gca ctc gcg gcc tta gcc aag aag tac ggg 192
Gly Pro Ile Pro His His Ala Leu Ala Ala Leu Ala Lys Lys Tyr Gly
50 55 60

cca ttg atg cac ctg cgg ctc ggg tgt gtg gac gtg gtt gtg gcc gcg 240
Pro Leu Met His Leu Arg Leu Gly Cys Val Asp Val Val Val Ala Ala
65 70 75

tct gct tcc gta gct gca cag ttt tta aaa gtt cac gac gca aat ttt 288
Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Val His Asp Ala Asn Phe
80 85 90 95

gct agt agg ccg cca aat tct ggc gcg aaa cat gtg gcg tat aat tat 336
Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr
100 105 110

cag gat ctt gtg ttt gca cct tat ggt cca agg tgg cgt ttg tta agg 384
Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Leu Leu Arg
115 120 125

aag att tgt tcg gtc cat ttg ttt tct gct aaa gca ctt gat gat ttt 432
Lys Ile Cys Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe
130 135 140

cgt cat gtt cga cag gag gag gta gca gtc cta acc cgc gta cta ctg 480
Arg His Val Arg Gln Glu Val Ala Val Leu Thr Arg Val Leu Leu
145 150 155

agt gct gga aac tca ccg gta cag ctt ggc caa cta ctt aac gtg tgt 528
Ser Ala Gly Asn Ser Pro Val Gln Leu Gly Gln Leu Leu Asn Val Cys
160 165 170 175

gcc aca aac gcc tta gca cgg gta atg tta ggt agg aga gtt ttc gga -- 576
Ala Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Arg Val Phe Gly
180 185 190

gac gga att gac agg tca gcc aat gag ttc aaa gat atg gta gta gag 624
Asp Gly Ile Asp Arg Ser Ala Asn Glu Phe Lys Asp Met Val Val Glu
195 200 205

tta atg gta tta gca gga gaa ttt aac ctt ggt gac ttt att cct gta		672	
Leu Met Val Leu Ala Gly Glu Phe Asn Leu Gly Asp Phe Ile Pro Val			
210	215	220	
ctt gac cta ttc gac cta caa ggc att act aaa aaa atg aag aag ctt		720	
Leu Asp Leu Phe Asp Leu Gln Gly Ile Thr Lys Lys Met Lys Lys Leu			
225	230	235	
cat gtt cgg ttc gat tca ttt ctt agt aag atc gtt gag gag cat aaa		768	
His Val Arg Phe Asp Ser Phe Leu Ser Lys Ile Val Glu Glu His Lys			
240	245	250	255
acg gca cct ggt ggg ttg ggt cat act gat ttg ctg agc acg ttg att		816	
Thr Ala Pro Gly Gly Leu Gly His Thr Asp Leu Leu Ser Thr Leu Ile			
260	265	270	
tca ctt aaa gat gat gct gat att gaa ggt ggg aag ctt aca gat act		864	
Ser Leu Lys Asp Asp Ala Asp Ile Glu Gly Gly Lys Leu Thr Asp Thr			
275	280	285	
gaa atc aaa gct ttg ctt ctg aat tta ttc gct gcg gga aca gac aca		912	
Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Ala Ala Gly Thr Asp Thr			
290	295	300	
tcc tct agt aca gta gaa tgg gca ata gcc gaa ctc att cgt cat cca		960	
Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg His Pro			
305	310	315	
caa ata tta aaa caa gcc cga gaa gag ata gac gct gta gtt ggt caa		1008	
Gln Ile Leu Lys Gln Ala Arg Glu Glu Ile Asp Ala Val Val Gly Gln			
320	325	330	335
gac cgg ctt gta aca gaa ttg gac ttg agc caa cta aca tac ctc cag		1056	
Asp Arg Leu Val Thr Glu Leu Asp Leu Ser Gln Leu Thr Tyr Leu Gln			
340	345	350	
gct ctt gtg aaa gag gtg ttt agg ctc cac cct tca acg cca ctc tcc		1104	
Ala Leu Val Lys Glu Val Phe Arg Leu His Pro Ser Thr Pro Leu Ser			
355	360	365	
tta cca aga ata tca tcc gag agt tgt gag gtc gat ggg tat tat atc		1152	
Leu Pro Arg Ile Ser Ser Glu Ser Cys Glu Val Asp Gly Tyr Tyr Ile			
370	375	380	
cct aag gga tcc aca ctc ctc gtt aac gtg tgg gcc att gcg cga gac		1200	
Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp			
385	390	395	
cca aaa atg tgg gcg gat cct ctt gaa ttt agg cct tct cgg ttt tta		1248	
Pro Lys Met Trp Ala Asp Pro Leu Glu Phe Arg Pro Ser Arg Phe Leu			
400	405	410	415
ccc ggg gga gaa aag ccc ggt gct gat gtt agg gga aat gat ttt gaa		1296	
Pro Gly Gly Lys Pro Gly Ala Asp Val Arg Gly Asn Asp Phe Glu			
420	425	430	
gtt ata cca ttt ggg gca gga cga agg att tgt gcg ggt atg agc cta		1344	
Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu			
435	440	445	

ggc ttg aga atg gtc cag ttg ctc att gca aca ttg gtc caa act ttt		1392	
Gly Leu Arg Met Val Gln Leu Leu Ile Ala Thr Leu Val Gln Thr Phe			
450	455	460	
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Asp Trp Glu Leu Ala Asn Gly Leu Glu Pro Glu Met Leu Asn Met Glu			
465	470	475	
gaa gcg tat gga ttg acc ctt caa cgg gct gca ccc ttg atg gtt cac		1488	
Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val His			
480	485	490	495
ccg aag ccg agg tta gct ccc cac gta tat gaa agt att taa		1530	
Pro Lys Pro Arg Leu Ala Pro His Val Tyr Glu Ser Ile			
500	505		
ggactagttt ctctttgcc ttttgtttc gcaaaggta atgaataaac gatttcatga	1590		
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aaaaaaaaaaa		1660	
<210> 17			
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<213> Chrysanthemum			
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Pro Gly Pro Thr Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu Gly			
35 40 45			
Pro Ile Pro His His Ala Leu Ala Ala Leu Ala Lys Lys Tyr Gly Pro			
50 55 60			
Leu Met His Leu Arg Leu Gly Cys Val Asp Val Val Val Ala Ala Ser			
65 70 75 80			
Ala Ser Val Ala Ala Gln Phe Leu Lys Val His Asp Ala Asn Phe Ala			
85 90 95			
Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr Gln			
100 105 110			
Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys			
115 120 125			
Ile Cys Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe Arg			
130 135 140			
His Val Arg Gln Glu Glu Val Ala Val Leu Thr Arg Val Leu Leu Ser			
145 150 155 160			
Ala Gly Asn Ser Pro Val Gln Leu Gly Gln Leu Leu Asn Val Cys Ala			
165 170 175			
Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Arg Val Phe Gly Asp			
180 185 190			
Gly Ile Asp Arg Ser Ala Asn Glu Phe Lys Asp Met Val Val Glu Leu			
195 200 205			
Met Val Leu Ala Gly Glu Phe Asn Leu Gly Asp Phe Ile Pro Val Leu			
210 215 220			
Asp Leu Phe Asp Leu Gln Gly Ile Thr Lys Lys Met Lys Lys Leu His			
225 230 235 240			

Val Arg Phe Asp Ser Phe Leu Ser Lys Ile Val Glu Glu His Lys Thr
 245 250 255
 Ala Pro Gly Gly Leu Gly His Thr Asp Leu Leu Ser Thr Leu Ile Ser
 260 265 270
 Leu Lys Asp Asp Ala Asp Ile Glu Gly Gly Lys Leu Thr Asp Thr Glu
 275 280 285
 Ile Lys Ala Leu Leu Leu Asn Leu Phe Ala Ala Gly Thr Asp Thr Ser
 290 295 300
 Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg His Pro Gln
 305 310 315 320
 Ile Leu Lys Gln Ala Arg Glu Glu Ile Asp Ala Val Val Gly Gln Asp
 325 330 335
 Arg Leu Val Thr Glu Leu Asp Leu Ser Gln Leu Thr Tyr Leu Gln Ala
 340 345 350
 Leu Val Lys Glu Val Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu
 355 360 365
 Pro Arg Ile Ser Ser Glu Ser Cys Glu Val Asp Gly Tyr Tyr Ile Pro
 370 375 380
 Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro
 385 390 395 400
 Lys Met Trp Ala Asp Pro Leu Glu Phe Arg Pro Ser Arg Phe Leu Pro
 405 410 415
 Gly Gly Glu Lys Pro Gly Ala Asp Val Arg Gly Asn Asp Phe Glu Val
 420 425 430
 Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly
 435 440 445
 Leu Arg Met Val Gln Leu Leu Ile Ala Thr Leu Val Gln Thr Phe Asp
 450 455 460
 Trp Glu Leu Ala Asn Gly Leu Glu Pro Glu Met Leu Asn Met Glu Glu
 465 470 475 480
 Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val His Pro
 485 490 495
 Lys Pro Arg Leu Ala Pro His Val Tyr Glu Ser Ile
 500 505

<210> 18
 <211> 1815
 <212> DNA
 <213> Torenia

<220>
 <221> CDS
 <222> (107)..(1633)

<400> 18
 ctaaaataat taataaatac acacacgacg agatgtatgt aatgtaatgt aatattatta 60

catacatcat caccgaatac gcacgctact accactgcga tttagcc atg agt ccc 115
 Met Ser Pro
 1

tta gcc ttg atg atc ata agt acc tta tta ggg ttt ctc cta tac cac 163
 Leu Ala Leu Met Ile Ile Ser Thr Leu Leu Gly Phe Leu Leu Tyr His
 5 10 15

tct ctt cgc tta cta ctc ttc tcc ggc caa ggt cgc cga cta cta cca 211

Ser	Leu	Arg	Leu	Leu	Leu	Phe	Ser	Gly	Gln	Gly	Arg	Arg	Leu	Leu	Pro	
20						25					30				35	
cca	ggt	cca	cgc	ccg	tgg	ccg	ctg	gtg	gga	aat	ctc	ccg	cac	tta	ggc	
Pro	Gly	Pro	Arg	Pro	Trp	Pro	Leu	Val	Gly	Asn	Leu	Pro	His	Leu	Gly	
						40				45					50	
ccg	aag	cca	cac	gcc	tcc	atg	gcc	gag	ctc	gcf	cga	gcc	tac	gga	ccc	
Pro	Lys	Pro	His	Ala	Ser	Met	Ala	Glu	Leu	Ala	Arg	Ala	Tyr	Gly	Pro	
						55			60			65				
ctc	atg	cac	cta	aag	atg	ggg	tcc	gtc	cac	gtc	gtg	gtg	gct	tcg	tcg	
Leu	Met	His	Leu	Lys	Met	Gly	Phe	Val	His	Val	Val	Val	Val	Ala	Ser	Ser
						70			75			80				
gcg	agc	gcf	gcf	gag	cag	tgc	ctg	agg	gtt	cac	gac	gcf	aat	ttc	ttg	
Ala	Ser	Ala	Ala	Glu	Gln	Cys	Leu	Arg	Val	His	Asp	Ala	Asn	Phe	Leu	
						85			90			95				
agc	agg	cca	ccc	aac	tcc	ggc	gcc	aag	cac	gtc	gct	tac	aac	tac	gag	
Ser	Arg	Pro	Pro	Asn	Ser	Gly	Ala	Lys	His	Val	Ala	Tyr	Asn	Tyr	Glu	
						100			105			110			115	
gac	ttg	gtt	tcc	aga	ccg	tac	ggf	ccc	aag	tgg	agg	ctg	ttg	agg	aag	
Asp	Leu	Val	Phe	Arg	Pro	Tyr	Gly	Pro	Lys	Trp	Arg	Leu	Leu	Arg	Lys	
						120			125			130				
ata	tgc	gct	cag	cat	att	tcc	gtc	aag	gct	atg	gat	gac	ttc	agg		
Ile	Cys	Ala	Gln	His	Ile	Phe	Ser	Val	Lys	Ala	Met	Asp	Asp	Phe	Arg	
						135			140			145				
cgf	gtc	aga	gag	gaa	gag	gtg	gcc	atc	ctg	agt	cgc	gct	cta	gca	ggc	
Arg	Val	Arg	Glu	Glu	Glu	Val	Ala	Ile	Leu	Ser	Arg	Ala	Leu	Ala	Gly	
						150			155			160				
aaa	agg	gcc	gta	ccc	ata	ggc	caa	atg	ctc	aac	gtg	tgc	gcc	aca	aac	
Lys	Arg	Ala	Val	Pro	Ile	Gly	Gln	Met	Leu	Asn	Val	Cys	Ala	Thr	Asn	
						165			170			175				
gcc	cta	tct	cgc	gtc	atg	atg	ggg	cgf	cgc	gtg	gtg	ggc	cac	gcf	gat	
Ala	Leu	Ser	Arg	Val	Met	Met	Gly	Arg	Arg	Val	Val	Gly	His	Ala	Asp	
						180			185			190			195	
gga	acc	aac	gac	gcc	aag	gcf	gag	gag	ttc	aaa	gcc	atg	gtc	gtc	gag	
Gly	Thr	Asn	Asp	Ala	Lys	Ala	Glu	Glu	Phe	Lys	Ala	Met	Val	Val	Glu	
						200			205			210				
ctc	atg	gtc	ctc	tcc	ggc	gtc	tcc	aac	atc	ggf	gat	ttc	atc	ccc	ttc	
Leu	Met	Val	Leu	Ser	Gly	Val	Phe	Asn	Ile	Gly	Asp	Phe	Ile	Pro	Phe	
						215			220			225				
ctc	gag	cct	ctc	gac	ttg	cag	gga	gtg	gct	tcc	aag	atg	aag	aaa	ctc	
Leu	Glu	Pro	Leu	Asp	Leu	Gln	Gly	Val	Ala	Ser	Lys	Met	Lys	Lys	Leu	
						230			235			240				
cac	gcf	cgf	ttc	gat	gca	ttc	ttg	acc	gag	att	gta	cga	gag	cgt	tgt	
His	Ala	Arg	Phe	Asp	Ala	Phe	Leu	Thr	Glu	Ile	Val	Arg	Glu	Arg	Cys	
						245			250			255				

cat ggg cag atc aac aac agt ggt gct cat cag gat gat ttg ctt agc His Gly Gln Ile Asn Asn Ser Ser Gly Ala His Gln Asp Asp Leu Leu Ser 260 265 270 275	931
acg ttg att tcg ttc aaa ggg ctt gac gat ggc gat ggt tcc agg ctc Thr Leu Ile Ser Phe Lys Gly Leu Asp Asp Gly Asp Gly Ser Arg Leu 280 285 290	979
act gac aca gaa atc aag gcg ctg ctc ttg aac ctt ttg gac acg acg Thr Asp Thr Glu Ile Lys Ala Leu Leu Asn Leu Leu Asp Thr Thr 295 300 305	1027
tcg agc acg gtg gaa tgg gcc gta gcc gaa ctc cta cgc cac cct aag Ser Ser Thr Val Glu Trp Ala Val Ala Glu Leu Leu Arg His Pro Lys 310 315 320	1075
aca tta gcc caa gtc cg ^g caa gag ctc gac tcg gtc gtg ggt aag aac Thr Leu Ala Gln Val Arg Gln Glu Leu Asp Ser Val Val Gly Lys Asn 325 330 335	1123
agg ctc gtg tcc gag acc gat ctg aat cag ctg ccc tat cta caa gct Arg Leu Val Ser Glu Thr Asp Leu Asn Gln Leu Pro Tyr Leu Gln Ala 340 345 350 355	1171
gtc gtc aaa gaa act ttc cgc ctc cat cct ccg acg ccg ctc tct cta Val Val Lys Glu Thr Phe Arg Leu His Pro Pro Thr Pro Leu Ser Leu 360 365 370	1219
ccg aga ctc gc ^g gaa gat gat tgc gag atc gac gga tac ctc atc ccc Pro Arg Leu Ala Glu Asp Asp Cys Glu Ile Asp Gly Tyr Leu Ile Pro 375 380 385	1267
aag ggc tcg acc ctt ctg gtg aac gtt tgg gcc ata gcc cgc gat ccc Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro 390 395 400	1315
aag gtt tgg gcc gat ccg ttg gag ttt agg ccc gaa cga ttc ttg acg Lys Val Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Leu Thr 405 410 415	1363
ggc gga gaa aag gcc gac gtc gat gtc aag ggg aac gat ttc gaa gtg Gly Gly Glu Lys Ala Asp Val Asp Val Lys Gly Asn Asp Phe Glu Val 420 425 430 435	1411
ata ccg ttc ggg gc ^g ggt cgt agg atc tgc gct ggc gtt ggc ttg gga Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Val Gly Leu Gly 440 445 450	1459
ata cgt atg gtc caa ctg ttg acg gc ^g agt ttg atc cat gca ttc gat Ile Arg Met Val Gln Leu Leu Thr Ala Ser Leu Ile His Ala Phe Asp 455 460 465	1507
ctg gac ctt gct aat ggg ctt ttg gcc caa aat ctg aac atg gaa gaa Leu Asp Leu Ala Asn Gly Leu Leu Ala Gln Asn Leu Asn Met Glu Glu 470 475 480	1555
gca tat ggg ctt acg cta caa cg ^g gct gag cct ttg ttg gtc cac cct Ala Tyr Gly Leu Thr Leu Gln Arg Ala Glu Pro Leu Leu Val His Pro 485 490 495	1603

agg ccg cggtt ggc act cat gtc tat taa tttaattttt cctaaactac 1653
Arg Pro Arg Leu Ala Thr His Val Tyr
500 505

gatgaatgac ccatttaacg ttaataagag ttttcaattt atgtgagttt gcatggtagt 1713
gtatggtagt gtgcttgtaa taaattgtat ctgttaggtg tgttcattga tgataaatct 1773
agtttgtact gctgctaaa aaaaaaaaaa aaaaaaaaaa aa 1815

<210> 19
<211> 508
<212> PRT
<213> Torenia

<400> 19

Met Ser Pro Leu Ala Leu Met Ile Ile Ser Thr Leu Leu Gly Phe Leu
1 5 10 15
Leu Tyr His Ser Leu Arg Leu Leu Phe Ser Gly Gln Gly Arg Arg
20 25 30
Leu Leu Pro Pro Gly Pro Arg Pro Trp Pro Leu Val Gly Asn Leu Pro
35 40 45
His Leu Gly Pro Lys Pro His Ala Ser Met Ala Glu Leu Ala Arg Ala
50 55 60
Tyr Gly Pro Leu Met His Leu Lys Met Gly Phe Val His Val Val Val
65 70 75 80
Ala Ser Ser Ala Ser Ala Ala Glu Gln Cys Leu Arg Val His Asp Ala
85 90 95
Asn Phe Leu Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr
100 105 110
Asn Tyr Glu Asp Leu Val Phe Arg Pro Tyr Gly Pro Lys Trp Arg Leu
115 120 125
Leu Arg Lys Ile Cys Ala Gln His Ile Phe Ser Val Lys Ala Met Asp
130 135 140
Asp Phe Arg Arg Val Arg Glu Glu Val Ala Ile Leu Ser Arg Ala
145 150 155 160
Leu Ala Gly Lys Arg Ala Val Pro Ile Gly Gln Met Leu Asn Val Cys
165 170 175
Ala Thr Asn Ala Leu Ser Arg Val Met Met Gly Arg Arg Val Val Gly
180 185 190

His Ala Asp Gly Thr Asn Asp Ala Lys Ala Glu Glu Phe Lys Ala Met
195 200 205
Val Val Glu Leu Met Val Leu Ser Gly Val Phe Asn Ile Gly Asp Phe
210 215 220
Ile Pro Phe Leu Glu Pro Leu Asp Leu Gln Gly Val Ala Ser Lys Met
225 230 235 240
Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Glu Ile Val Arg
245 250 255
Glu Arg Cys His Gly Gln Ile Asn Asn Ser Gly Ala His Gln Asp Asp
260 265 270
Leu Leu Ser Thr Leu Ile Ser Phe Lys Gly Leu Asp Asp Gly Asp Gly
275 280 285
Ser Arg Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Asn Leu Leu
290 295 300
Asp Thr Thr Ser Ser Thr Val Glu Trp Ala Val Ala Glu Leu Leu Arg
305 310 315 320
His Pro Lys Thr Leu Ala Gln Val Arg Gln Glu Leu Asp Ser Val Val
325 330 335

Gly Lys Asn Arg Leu Val Ser Glu Thr Asp Leu Asn Gln Leu Pro Tyr
 340 345 350
 Leu Gln Ala Val Val Lys Glu Thr Phe Arg Leu His Pro Pro Thr Pro
 355 360 365
 Leu Ser Leu Pro Arg Leu Ala Glu Asp Asp Cys Glu Ile Asp Gly Tyr
 370 375 380
 Leu Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala
 385 390 395 400
 Arg Asp Pro Lys Val Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg
 405 410 415
 Phe Leu Thr Gly Gly Lys Ala Asp Val Asp Val Lys Gly Asn Asp
 420 425 430
 Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Val
 435 440 445
 Gly Leu Gly Ile Arg Met Val Gln Leu Leu Thr Ala Ser Leu Ile His
 450 455 460
 Ala Phe Asp Leu Asp Leu Ala Asn Gly Leu Leu Ala Gln Asn Leu Asn
 465 470 475 480
 Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Glu Pro Leu Leu
 485 490 495
 Val His Pro Arg Pro Arg Leu Ala Thr His Val Tyr
 500 505

<210> 20
 <211> 1824
 <212> DNA
 <213> Jap. Morning Glory

<220>
 <221> CDS
 <222> (2)..(1555)

<400> 20
 g agc tta acc tta att ttc tgc act tta gtt ttt gca atc ttt cta tat 49
 Ser Leu Thr Leu Ile Phe Cys Thr Leu Val Phe Ala Ile Phe Leu Tyr
 1 5 10 15
 ttt ctt att ctc agg gtg aaa cag cgt tac cct ctc cca ccc 97
 Phe Leu Ile Leu Arg Val Lys Gln Arg Tyr Pro Leu Pro Leu Pro
 20 25 30
 gga cca aaa cca tgg ccg gtg tta gga aac ctt ccc cac ctg ggc aag 145
 Gly Pro Lys Pro Trp Pro Val Leu Gly Asn Leu Pro His Leu Gly Lys
 35 40 45
 aag cct cac cag tcg att gcg gcc atg gct gag agg tac ggc ccc ctc 193
 Lys Pro His Gln Ser Ile Ala Ala Met Ala Glu Arg Tyr Gly Pro Leu
 50 55 60
 atg cac ctc cgc cta gga ttc gtg gac gtg gtt gtg gcc gcc tcc gcc 241
 Met His Leu Arg Leu Gly Phe Val Asp Val Val Ala Ala Ser Ala
 65 70 75 80
 gcc gtg gcc gct cag ttc ttg aaa gtt cac gac tcg aac ttc tcc aac 289
 Ala Val Ala Ala Gln Phe Leu Lys Val His Asp Ser Asn Phe Ser Asn
 85 90 95
 cgg ccg ccg aac tcc ggc gcg gaa cac att gct tat aac tat caa gac 337

Arg	Pro	Pro	Asn	Ser	Gly	Ala	Glu	His	Ile	Ala	Tyr	Asn	Tyr	Gln	Asp		
100							105							110			
ctc	gtc	ttc	gcf	ccc	tac	ggc	ccg	cgf	tgg	cgc	atg	ctt	agg	aag	atc	385	
Leu	Val	Phe	Ala	Pro	Tyr	Gly	Pro	Arg	Trp	Arg	Met	Leu	Arg	Lys	Ile		
115							120							125			
acc	tcc	gtg	cat	ctc	ttc	tcg	gcc	aag	gcf	ttg	gat	gac	ttc	tgc	cat	433	
Thr	Ser	Val	His	Leu	Phe	Ser	Ala	Lys	Ala	Leu	Asp	Asp	Phe	Cys	His		
130							135							140			
gtt	cgc	cag	gaa	gag	gtt	gca	act	ctg	aca	cgc	agt	cta	gca	agt	gca	481	
Val	Arg	Gln	Glu	Glu	Val	Ala	Thr	Leu	Thr	Arg	Ser	Leu	Ala	Ser	Ala		
145							150							155			160
ggc	aaa	act	cca	gta	aaa	cta	ggg	cag	tta	cta	aac	gtg	tgc	acc	acg	529	
Gly	Lys	Thr	Pro	Val	Lys	Leu	Gly	Gln	Leu	Leu	Asn	Val	Cys	Thr	Thr		
							165							175			
aac	gcc	cta	gct	cgt	gta	atg	ctt	ggg	cgf	aag	gtc	ttt	aat	gac	gga	577	
Asn	Ala	Leu	Ala	Arg	Val	Met	Leu	Gly	Arg	Lys	Val	Phe	Asn	Asp	Gly		
							180							185			190
ggf	agc	aag	agc	gac	cca	aag	gcf	gag	gag	ttc	aag	tcg	atg	gtg	gag	625	
Gly	Ser	Lys	Ser	Asp	Pro	Lys	Ala	Glu	Glu	Phe	Lys	Ser	Met	Val	Glu		
							195							200			205
gag	atg	atg	gtg	ttt	gcc	gga	agt	ttt	aac	atc	ggc	gat	ttc	att	ccg	673	
Glu	Met	Met	Val	Leu	Ala	Gly	Ser	Phe	Asn	Ile	Gly	Asp	Phe	Ile	Pro		
							210							215			220
gtc	ttt	ggf	tgg	ttt	gac	gtt	cag	ggf	atc	gta	ggg	aag	atg	aag	aaa	721	
Val	Leu	Gly	Trp	Phe	Asp	Val	Gln	Gly	Ile	Val	Gly	Lys	Met	Lys	Lys		
							225							230			235
ctt	cac	gcf	cgt	ttt	gat	gcf	ttc	ttt	aac	acc	att	cta	gag	gaa	cac	769	
Leu	His	Ala	Arg	Phe	Asp	Ala	Phe	Leu	Asn	Thr	Ile	Leu	Glu	Glu	His		
							245							250			255
aaa	tgt	gtc	aac	aat	caa	cac	acg	acg	ttt	tcg	aaa	gat	gtg	gac	ttc	817	
Lys	Cys	Val	Asn	Asn	Gln	His	Thr	Thr	Leu	Ser	Lys	Asp	Val	Asp	Phe		
							260							265			270
ttt	agc	acc	cta	att	agg	ctc	aaa	gat	aat	ggg	gct	gat	atg	gat	tgt	865	
Leu	Ser	Thr	Leu	Ile	Arg	Leu	Lys	Asp	Asn	Gly	Ala	Asp	Met	Asp	Cys		
							275							280			285
gaa	gag	gga	aaa	ctc	acc	gac	act	gaa	att	aag	gct	ttt	tcg	ttt	aac	913	
Glu	Glu	Gly	Lys	Leu	Thr	Asp	Thr	Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn		
							290							295			300
ctg	tcc	aca	gct	ggg	act	gat	aca	tca	tct	agc	act	gtg	gag	tgg	gca	961	
Leu	Phe	Thr	Ala	Gly	Thr	Asp	Thr	Ser	Ser	Ser	Ser	Thr	Val	Glu	Trp		
							305							310			315
atc	gca	gaa	cta	cta	cgc	aac	cca	aaa	atc	tta	aac	caa	gca	caa	caa	1009	
Ile	Ala	Glu	Leu	Leu	Arg	Asn	Pro	Lys	Ile	Leu	Asn	Gln	Ala	Gln	Gln		
							325							330			335
gag	ctt	gac	tta	gtg	gtg	ggt	caa	aat	cag	cta	gtc	aca	gaa	tct	gac	1057	

<210> 21
<211> 517
<212> PRT

<213> Jap. Morning Glory

<400> 21

Ser Leu Thr Leu Ile Phe Cys Thr Leu Val Phe Ala Ile Phe Leu Tyr
1 5 10 15
Phe Leu Ile Leu Arg Val Lys Gln Arg Tyr Pro Leu Pro Leu Pro Pro
20 25 30
Gly Pro Lys Pro Trp Pro Val Leu Gly Asn Leu Pro His Leu Gly Lys
35 40 45
Lys Pro His Gln Ser Ile Ala Ala Met Ala Glu Arg Tyr Gly Pro Leu
50 55 60
Met His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala Ala Ser Ala
65 70 75 80
Ala Val Ala Ala Gln Phe Leu Lys Val His Asp Ser Asn Phe Ser Asn
85 90 95
Arg Pro Pro Asn Ser Gly Ala Glu His Ile Ala Tyr Asn Tyr Gln Asp
100 105 110
Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys Ile
115 120 125
Thr Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe Cys His
130 135 140
Val Arg Gln Glu Glu Val Ala Thr Leu Thr Arg Ser Leu Ala Ser Ala
145 150 155 160

Gly Lys Thr Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr Thr
165 170 175
Asn Ala Leu Ala Arg Val Met Leu Gly Arg Lys Val Phe Asn Asp Gly
180 185 190
Gly Ser Lys Ser Asp Pro Lys Ala Glu Glu Phe Lys Ser Met Val Glu
195 200 205
Glu Met Met Val Leu Ala Gly Ser Phe Asn Ile Gly Asp Phe Ile Pro
210 215 220
Val Leu Gly Trp Phe Asp Val Gln Gly Ile Val Gly Lys Met Lys Lys
225 230 235 240
Leu His Ala Arg Phe Asp Ala Phe Leu Asn Thr Ile Leu Glu Glu His
245 250 255
Lys Cys Val Asn Asn Gln His Thr Thr Leu Ser Lys Asp Val Asp Phe
260 265 270
Leu Ser Thr Leu Ile Arg Leu Lys Asp Asn Gly Ala Asp Met Asp Cys
275 280 285
Glu Glu Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn
290 295 300
Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp Ala
305 310 315 320
Ile Ala Glu Leu Leu Arg Asn Pro Lys Ile Leu Asn Gln Ala Gln Gln
325 330 335
Glu Leu Asp Leu Val Val Gly Gln Asn Gln Leu Val Thr Glu Ser Asp
340 345 350
Leu Thr Asp Leu Pro Phe Leu Gln Ala Ile Val Lys Glu Thr Phe Arg
355 360 365
Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Gly Ala Gln Gly
370 375 380
Cys Glu Ile Asn Gly Tyr Phe Ile Pro Lys Gly Ala Thr Leu Leu Val
385 390 395 400
Asn Val Trp Ala Ile Ala Arg Asp Pro Asn Val Trp Thr Asn Pro Leu
405 410 415
Glu Phe Asn Pro His Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val
420 425 430
Asp Ile Lys Gly Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg
435 440 445

Arg	Ile	Cys	Ser	Gly	Met	Ser	Leu	Gly	Ile	Arg	Met	Val	His	Leu	Leu
450				455						460					
Val	Ala	Thr	Leu	Val	His	Ala	Phe	Asp	Trp	Asp	Leu	Val	Asn	Gly	Gln
465				470						475				480	
Ser	Val	Glu	Thr	Leu	Asn	Met	Glu	Glu	Ala	Tyr	Gly	Leu	Thr	Leu	Gln
				485						490				495	
Arg	Ala	Val	Pro	Leu	Met	Leu	His	Pro	Lys	Pro	Arg	Leu	Gln	Pro	His
				500						505				510	
Leu	Tyr	Thr	Leu	Asn											
				515											

<210> 22
<211> 1667
<212> DNA
<213> Gentian

<220>
<221> CDS
<222> (1)..(1431)

<400> 22															
ccc	atc	ctc	gga	aac	atc	ccc	cat	ctc	ggc	tcc	aaa	ccg	cac	caa	aca
Pro	Ile	Leu	Gly	Asn	Ile	Pro	His	Leu	Gly	Ser	Lys	Pro	His	Gln	Thr
1					5					10					48
ctc	gca	gaa	atg	gca	aaa	acc	tac	ggt	ccg	ctc	atg	cac	ttg	aag	ttc
Leu	Ala	Glu	Met	Ala	Lys	Thr	Tyr	Gly	Pro	Leu	Met	His	Leu	Lys	Phe
					20					25					96
ggg	ctt	aag	gac	gca	gtg	gtg	gca	tcg	tct	gca	gtg	gca	gag	cag	
Gly	Leu	Lys	Asp	Ala	Val	Ala	Ser	Ser	Ala	Ser	Ala	Val	Ala	Glu	Gln
					35					40					144
ttt	ctg	aag	aaa	cac	gac	gtg	aat	ttc	tcg	aac	cg	ccg	cca	aac	tcc
Phe	Leu	Lys	Lys	His	Asp	Val	Asn	Phe	Ser	Asn	Arg	Pro	Pro	Asn	Ser
					50					55					192
ggg	gcc	aaa	cat	ata	gct	tat	aac	tat	cag	gac	ctg	gta	ttc	gct	ccc
Gly	Ala	Lys	His	Ile	Ala	Tyr	Asn	Tyr	Gln	Asp	Leu	Val	Phe	Ala	Pro
					65					70					240
tat	gga	ccc	cg	tgg	cg	ttg	ctt	agg	aaa	atc	tgt	tcc	gtc	cat	ctt
Tyr	Gly	Pro	Arg	Trp	Arg	Leu	Leu	Arg	Lys	Ile	Cys	Ser	Val	His	Leu
					85					90					288
ttc	tcg	tct	aag	gcc	ttg	gat	gac	ttt	cag	cat	gt	cga	cat	gag	gag
Phe	Ser	Ser	Lys	Ala	Leu	Asp	Asp	Phe	Gln	His	Val	Arg	His	Glu	Glu
					100					105					336
ata	tgc	atc	ctt	ata	cga	gca	ata	gca	agt	ggc	ggt	cat	gct	ccg	gtg
Ile	Cys	Ile	Leu	Ile	Arg	Ala	Ile	Ala	Ser	Gly	Gly	His	Ala	Pro	Val
					115					120					384
aat	tta	ggc	aag	tta	gg	gt	tg	tc	aca	acc	aat	ggc	ctg	gca	aga
Asn	Leu	Gly	Lys	Leu	Leu	Gly	Val	Cys	Thr	Thr	Asn	Ala	Leu	Ala	Arg
					130					135					432
gtg	atg	ctt	gga	aga	aga	gta	ttc	gaa	ggc	gac	ggc	ggc	gag	aat	ccg
															480

Val	Met	Leu	Gly	Arg	Arg	Val	Phe	Glu	Gly	Asp	Gly	Gly	Glu	Asn	Pro		
145						150				155				160			
cat	gcc	gac	gag	ttt	aaa	tca	atg	gtg	gtg	gag	att	atg	gtg	tta	gcc	528	
His	Ala	Asp	Glu	Phe	Lys	Ser	Met	Val	Val	Glu	Ile	Met	Val	Leu	Ala		
						165				170				175			
ggt	gca	ttc	aac	ttg	ggt	gat	ttc	atc	ccg	gtt	cta	gat	tgg	ttc	gat	576	
Gly	Ala	Phe	Asn	Leu	Gly	Asp	Phe	Ile	Pro	Val	Leu	Asp	Trp	Phe	Asp		
						180				185				190			
ttg	caa	gga	att	gct	ggt	aaa	atg	aag	aaa	ctt	cat	gcc	cgt	ttc	gac	624	
Leu	Gln	Gly	Ile	Ala	Gly	Lys	Met	Lys	Lys	Leu	His	Ala	Arg	Phe	Asp		
						195				200				205			
aag	ttt	tta	aat	ggg	atc	cta	gaa	gat	cgt	aaa	tct	aac	ggc	tct	aat	672	
Lys	Phe	Leu	Asn	Gly	Ile	Leu	Glu	Asp	Arg	Lys	Ser	Asn	Gly	Ser	Asn		
						210				215				220			
gga	gct	gaa	caa	tac	gtg	gac	ttg	ctc	agt	gtg	ttg	atc	tct	ctt	caa	720	
Gly	Ala	Glu	Gln	Tyr	Val	Asp	Leu	Leu	Ser	Val	Leu	Ile	Ser	Leu	Gln		
						225				230				235			240
gat	agt	aat	atc	gac	ggt	ggt	gac	gaa	gga	acc	aaa	ctc	aca	gat	act	768	
Asp	Ser	Asn	Ile	Asp	Gly	Gly	Asp	Glu	Gly	Thr	Lys	Leu	Thr	Asp	Thr		
						245				250				255			
gaa	atc	aaa	gct	ctc	ctt	ttg	aac	ttg	ttc	ata	gcc	gga	aca	gac	act	816	
Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn	Leu	Phe	Ile	Ala	Gly	Thr	Asp	Thr		
						260				265				270			
tca	tca	agt	act	gta	gaa	tgg	gcc	atg	gca	gaa	cta	atc	cga	aac	cca	864	
Ser	Ser	Ser	Thr	Val	Glu	Trp	Ala	Met	Ala	Glu	Leu	Ile	Arg	Asn	Pro		
						275				280				285			
aag	tta	cta	gtc	caa	gcc	caa	gaa	gag	cta	gac	aga	gta	gtc	ggg	ccg	912	
Lys	Leu	Leu	Val	Gln	Ala	Gln	Glu	Glu	Leu	Asp	Arg	Val	Val	Gly	Pro		
						290				295				300			
aac	cga	ttc	gta	acc	gaa	tct	gat	ctt	cct	caa	ctg	aca	ttc	ctt	caa	960	
Asn	Arg	Phe	Val	Thr	Glu	Ser	Asp	Leu	Pro	Gln	Leu	Thr	Phe	Leu	Gln		
						305				310				315			320
gcc	gtc	atc	aaa	gag	act	ttc	agg	ctt	cat	cca	tcc	acc	cca	ctc	tct	1008	
Ala	Val	Ile	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro	Leu	Ser		
						325				330				335			
ctt	cca	cga	atg	gcg	gag	gac	tgt	gag	atc	aat	ggg	tat	tat	gtc		1056	
Leu	Pro	Arg	Met	Ala	Ala	Glu	Asp	Cys	Glu	Ile	Asn	Gly	Tyr	Tyr	Val		
						340				345				350			
tca	gaa	ggt	tcg	aca	ttg	ctc	gtc	aat	gtg	tgg	gcc	ata	gct	cgt	gat	1104	
Ser	Glu	Gly	Ser	Thr	Leu	Leu	Val	Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp		
						355				360				365			
cca	aat	gct	tgg	gcc	aat	cca	cta	gat	ttc	aac	ccg	act	cgt	ttc	ttg	1152	
Pro	Asn	Ala	Trp	Ala	Asn	Pro	Leu	Asp	Phe	Asn	Pro	Thr	Arg	Phe	Leu		
						370				375				380			
gcc	ggt	gga	gag	aag	cct	aat	gtt	gat	gtt	aaa	ggg	aat	gat	ttt	gaa	1200	

Ala	Gly	Gly	Glu	Lys	Pro	Asn	Val	Asp	Val	Lys	Gly	Asn	Asp	Phe	Glu	
385				390						395				400		
gtg	ata	cct	ttc	ggg	gct	ggg	cgc	agg	ata	tgt	gcc	gga	atg	agc	tta	1248
Val	Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Met	Ser	Leu	
			405						410				415			
ggt	ata	cgg	atg	gtt	caa	cta	gta	acg	gct	tcg	tta	gtt	cat	tcg	ttt	1296
Gly	Ile	Arg	Met	Val	Gln	Leu	Val	Thr	Ala	Ser	Leu	Val	His	Ser	Phe	
			420						425				430			
gat	tgg	gct	ttg	ttg	gat	gga	ctt	aaa	ccc	gag	aag	ctt	gac	atg	gag	1344
Asp	Trp	Ala	Leu	Leu	Asp	Gly	Leu	Lys	Pro	Glu	Lys	Leu	Asp	Met	Glu	
		435					440					445				
gaa	ggt	tat	gga	cta	acg	ctt	caa	cga	gct	tca	cct	tta	atc	gtc	cat	1392
Glu	Gly	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Ser	Pro	Leu	Ile	Val	His	
		450				455					460					
cca	aag	ccg	agg	ctc	tcg	gct	caa	gtt	tat	tgt	atg	taa	caagtttg			1441
Pro	Lys	Pro	Arg	Leu	Ser	Ala	Gln	Val	Tyr	Cys	Met					
		465				470				475						
aagccagtct	gatttcagtt	ggattttag	ttatttatg	atcatttgg	attttattt											1501
gtatttcggt	tgaataacaat	aaaggaaagg	tggatcgct	gctgtataat	agcgacgtt											1561
taacgtgttg	tgatagtacc	gtgtttact	aaaacgatgt	cgtttgattt	tttatagtat											1621
aaaaaaaaata	aacagctgga	ttttgaacca	aaaaaaaaaaa	aaaaaaa												1667

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<211> 476
<212> PRT
<213> Gentian

<400> 23																
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Leu	Ala	Glu	Met	Ala	Lys	Thr	Tyr	Gly	Pro	Leu	Met	His	Leu	Lys	Phe	
						20			25			30				
Gly	Leu	Lys	Asp	Ala	Val	Val	Ala	Ser	Ser	Ala	Ser	Val	Ala	Glu	Gln	
							35		40			45				
Phe	Leu	Lys	Lys	His	Asp	Val	Asn	Phe	Ser	Asn	Arg	Pro	Pro	Asn	Ser	
						50		55			60					
Gly	Ala	Lys	His	Ile	Ala	Tyr	Asn	Tyr	Gln	Asp	Leu	Val	Phe	Ala	Pro	
						65		70			75			80		
Tyr	Gly	Pro	Arg	Trp	Arg	Leu	Leu	Arg	Lys	Ile	Cys	Ser	Val	His	Leu	
						85			90			95				
Phe	Ser	Ser	Lys	Ala	Leu	Asp	Asp	Phe	Gln	His	Val	Arg	His	Glu	Glu	
						100		105			110					
Ile	Cys	Ile	Leu	Ile	Arg	Ala	Ile	Ala	Ser	Gly	Gly	His	Ala	Pro	Val	
						115		120			125					
Asn	Leu	Gly	Lys	Leu	Leu	Gly	Val	Cys	Thr	Thr	Asn	Ala	Leu	Ala	Arg	
						130		135			140					
Val	Met	Leu	Gly	Arg	Arg	Val	Phe	Glu	Gly	Asp	Gly	Gly	Glu	Asn	Pro	
145					150				155				160			
His	Ala	Asp	Glu	Phe	Lys	Ser	Met	Val	Val	Glu	Ile	Met	Val	Leu	Ala	

165	170	175
Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Val Leu Asp Trp Phe Asp		
180	185	190
Leu Gln Gly Ile Ala Gly Lys Met Lys Lys Leu His Ala Arg Phe Asp		
195	200	205
Lys Phe Leu Asn Gly Ile Leu Glu Asp Arg Lys Ser Asn Gly Ser Asn		
210	215	220
Gly Ala Glu Gln Tyr Val Asp Leu Leu Ser Val Leu Ile Ser Leu Gln		
225	230	235
Asp Ser Asn Ile Asp Gly Gly Asp Glu Gly Thr Lys Leu Thr Asp Thr		
245	250	255
Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Ile Ala Gly Thr Asp Thr		
260	265	270
Ser Ser Ser Thr Val Glu Trp Ala Met Ala Glu Leu Ile Arg Asn Pro		
275	280	285
Lys Leu Leu Val Gln Ala Gln Glu Glu Leu Asp Arg Val Val Gly Pro		
290	295	300
Asn Arg Phe Val Thr Glu Ser Asp Leu Pro Gln Leu Thr Phe Leu Gln		
305	310	315
Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser		
325	330	335
Leu Pro Arg Met Ala Ala Glu Asp Cys Glu Ile Asn Gly Tyr Tyr Val		
340	345	350
Ser Glu Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp		
355	360	365
Pro Asn Ala Trp Ala Asn Pro Leu Asp Phe Asn Pro Thr Arg Phe Leu		
370	375	380
Ala Gly Gly Glu Lys Pro Asn Val Asp Val Lys Gly Asn Asp Phe Glu		
385	390	395
Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu		
405	410	415
Gly Ile Arg Met Val Gln Leu Val Thr Ala Ser Leu Val His Ser Phe		
420	425	430
Asp Trp Ala Leu Leu Asp Gly Leu Lys Pro Glu Lys Leu Asp Met Glu		
435	440	445
Glu Gly Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His		
450	455	460
Pro Lys Pro Arg Leu Ser Ala Gln Val Tyr Cys Met		
465	470	475

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<211> 1214
<212> DNA
<213> Lisianthus

<220>
<221> CDS
<222> (2)..(1093)

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Arg-Ile-Leu-Thr Arg-Ser-Ile-Ala-Ser-Ala-Gly-Glu-Asn-Pro-Ile-Asn
1 5 10 15

tta ggt caa tta ctc ggg gtg tgt acc aca aat gct ctg gcg aga gtg 97
Leu Gly Gln Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg Val
20 25 30

atg ctt gga agg agg gta ttc ggc gat ggg agc ggc ggc gta gat cct		145	
Met Leu Gly Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Val Asp Pro			
35	40	45	
cag gcg gac gag ttc aaa tcc atg gtg gaa atc atg gtg ttg gcc		193	
Gln Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala			
50	55	60	
ggc gcg ttt aat cta ggt gat ttt att ccc gct ctt gat tgg ttc gat		241	
Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Ala Leu Asp Trp Phe Asp			
65	70	75	80
ctg cag gga att acg gca aaa atg aag aaa gtt cac gct cgt ttc gat		289	
Leu Gln Gly Ile Thr Ala Lys Met Lys Lys Val His Ala Arg Phe Asp			
85	90	95	
gcu ttc tta gac gcu atc ctt gag qag cac aaa tcc aac qgc tct cgc		337	
Ala Phe Leu Asp Ala Ile Leu Glu Glu His Lys Ser Asn Gly Ser Arg			
100	105	110	
gga gct aag caa cac gtt gac ttg ctg agt atg ttg atc tcc ctt caa		385	
Gly Ala Lys Gln His Val Asp Leu Leu Ser Met Leu Ile Ser Leu Gln			
115	120	125	
gat aat aac att gat ggt gaa agt ggc gcc aaa ctc act gat aca gaa		433	
Asp Asn Asn Ile Asp Gly Glu Ser Gly Ala Lys Leu Thr Asp Thr Glu			
130	135	140	
atc aaa gct ttg ctt ctg aac ttg ttc acg gct gga aca gac acg tca		481	
Ile Lys Ala Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser			
145	150	155	160
tca agt act gtg gag tgg gca atc gca gag cta atc cga aac cca gaa		529	
Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn Pro Glu			
165	170	175	
gta ttg gtt caa gcc caa caa gag ctc gat aga gta gtt ggg cca agt		577	
Val Leu Val Gln Ala Gln Glu Leu Asp Arg Val Val Gly Pro Ser			
180	185	190	
cgt ctt gtg acc gaa tct gat ctg cct caa ttg gca ttc ctt caa gct		625	
Arg Leu Val Thr Glu Ser Asp Leu Pro Gln Leu Ala Phe Leu Gln Ala			
195	200	205	
gtc atc aaa gag act ttc aga ctt cat cca tcc act cca ctc tct ctt		673	
Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu			
210	215	220	
cca cga atg gct tca gag ggt tgt gaa atc aat gga tac tcc atc cca		721	
Pro Arg Met Ala Ser Glu Gly Cys Glu Ile Asn Gly Tyr Ser Ile Pro			
225	230	235	240
aag ggt tcg aca ttg ctc gtt aac gta tgg tcc ata gcc cgt gat cct		769	
Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ser Ile Ala Arg Asp Pro			
245	250	255	
agt ata tgg gcc gac cca tta gaa ttt agg ccg gca cgt ttc ttg ccc		817	
Ser Ile Trp Ala Asp Pro Leu Glu Phe Arg Pro Ala Arg Phe Leu Pro			
260	265	270	

ggc gga gaa aag ccc aat gtt gat gtg aga ggc aat gat ttt gag gtc		865	
Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly Asn Asp Phe Glu Val			
275	280	285	
ata cca ttt ggt gct gga cgt agg ata tgt gct gga atg agc ttg ggt		913	
Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly			
290	295	300	
tta aga atg gtt caa ctt tcg aca gct act ttg gtt cat tcg ttt aat		961	
Leu Arg Met Val Gln Leu Ser Thr Ala Thr Leu Val His Ser Phe Asn			
305	310	315	320
tgg gat ttg ctg aat ggg atg agc cca gat aaa ctt gac atg gaa gaa		1009	
Trp Asp Leu Leu Asn Gly Met Ser Pro Asp Lys Leu Asp Met Glu Glu			
325	330	335	
gct tat ggg ctt aca ttg caa cgg gct tca cct ttg att gtc cac cca		1057	
Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His Pro			
340	345	350	
aag ccc agg ctt gct agc tct atg tat gtt aaa tga aattatgctg		1103	
Lys Pro Arg Leu Ala Ser Ser Met Tyr Val Lys			
355	360		
tgcaataat tccttattta tagcaggaaa tgcatctt aattatgtgt aatgttcttc		1163	
taacttcga tgaaagtgc aaacaagttt tattaaaaaa aaaaaaaaaa a		1214	

<210> 25
<211> 363
<212> PRT
<213> Lisianthus

<400> 25
Arg Ile Leu Thr Arg Ser Ile Ala Ser Ala Gly Glu Asn Pro Ile Asn
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Leu Gly Gln Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg Val
20 25 30
Met Leu Gly Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Val Asp Pro
35 40 45
Gln Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala
50 55 60
Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Ala Leu Asp Trp Phe Asp
65 70 75 80
Leu Gln Gly Ile Thr Ala Lys Met Lys Lys Val His Ala Arg Phe Asp
85 90 95
Ala Phe Leu Asp Ala Ile Leu Glu Glu His Lys Ser Asn Gly Ser Arg
100 105 110
Gly Ala Lys Gln His Val Asp Leu Leu Ser Met Leu Ile Ser Leu Gln
115 120 125
Asp Asn Asn Ile Asp Gly Glu Ser Gly Ala Lys Leu Thr Asp Thr Glu
130 135 140
Ile Lys Ala Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser
145 150 155 160
Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn Pro Glu
165 170 175
Val Leu Val Gln Ala Gln Gln Glu Leu Asp Arg Val Val Gly Pro Ser
180 185 190
Arg Leu Val Thr Glu Ser Asp Leu Pro Gln Leu Ala Phe Leu Gln Ala

195	200	205
Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu		
210	215	220
Pro Arg Met Ala Ser Glu Gly Cys Glu Ile Asn Gly Tyr Ser Ile Pro		
225	230	235
Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ser Ile Ala Arg Asp Pro		
245	250	255
Ser Ile Trp Ala Asp Pro Leu Glu Phe Arg Pro Ala Arg Phe Leu Pro		
260	265	270
Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly Asn Asp Phe Glu Val		
275	280	285
Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly		
290	295	300
Leu Arg Met Val Gln Leu Ser Thr Ala Thr Leu Val His Ser Phe Asn		
305	310	315
Trp Asp Leu Leu Asn Gly Met Ser Pro Asp Lys Leu Asp Met Glu Glu		
325	330	335
Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His Pro		
340	345	350
Lys Pro Arg Leu Ala Ser Ser Met Tyr Val Lys		
355	360	

<210> 26
<211> 1757
<212> DNA
<213> Petunia sp.

<220>
<221> CDS
<222> (35)..(1525)

<400> 26
ccgttgctgt cgagaaaaaca gaaagaagag aaaa atg gac tac gtg aat att ttg 55
Met Asp Tyr Val Asn Ile Leu
1 5

ctg gga ctg ttt ttc act tgg ttc ttg gtg aat gga ctc atg tca ctt 103
Leu Gly Leu Phe Phe Thr Trp Phe Leu Val Asn Gly Leu Met Ser Leu
10 15 20

cga aga aga aaa atc tct aag aaa ctt cca cca ggt cca ttt cct ttg 151
Arg Arg Arg Lys Ile Ser Lys Lys Leu Pro Pro Gly Pro Phe Pro Leu
25 30 35

cct atc atc gga aat ctt cac tta ctt ggt aat cat cct cac aaa tca 199
Pro Ile Ile Gly Asn Leu His Leu Leu Gly Asn His Pro His Lys Ser
40 45 50 55

ctt gct caa ctt gca aaa att cat ggt cct att atg aat ctc aaa tta 247
Leu Ala Gln Leu Ala Lys Ile His Gly Pro Ile Met Asn Leu Lys Leu
60 65 70

ggc caa cta aac aca gtg gtc att tca tca tca gtc gtg gca aga gaa 295
Gly Gln Leu Asn Thr Val Val Ile Ser Ser Ser Val Val Ala Arg Glu
75 80 85

gtc ttg caa aaa caa gac tta aca ttt tcc aat agg ttt gtc ccg gac 343
Val Leu Gln Lys Gln Asp Leu Thr Phe Ser Asn Arg Phe Val Pro Asp

90	95	100	
gta gtc cat gtc cga aat cac tcc gat ttt tct gtt gtt tgg tta cca Val Val His Val Arg Asn His Ser Asp Phe Ser Val Val Trp Leu Pro 105 110 115			391
gtc aat tct cga tgg aaa acg ctt cgc aaa atc atg aac tct agc atc Val Asn Ser Arg Trp Lys Thr Leu Arg Lys Ile Met Asn Ser Ser Ile 120 125 130 135			439
ttt tct ggt aac aag ctt gat ggt aat caa cat ctg agg tct aaa aag Phe Ser Gly Asn Lys Leu Asp Gly Asn Gln His Leu Arg Ser Lys Lys 140 145 150			487
gtc caa gag tta att gat tat tgt caa aag tgt gcc aag aat ggc gaa Val Gln Glu Leu Ile Asp Tyr Cys Gln Lys Cys Ala Lys Asn Gly Glu 155 160 165			535
gca gtg gat ata gga aga gca act ttt gga act act ttg aat ttg cta Ala Val Asp Ile Gly Arg Ala Thr Phe Gly Thr Thr Leu Asn Leu Leu 170 175 180			583
tcc aac acc att ttc tct aaa gat ttg act aat ccg ttt tct gat tct Ser Asn Thr Ile Phe Ser Lys Asp Leu Thr Asn Pro Phe Ser Asp Ser 185 190 195			631
gct aaa gag ttt aag gaa ttg gtt tgg aac att atg gtt gag gct gga Ala Lys Glu Phe Lys Glu Leu Val Trp Asn Ile Met Val Glu Ala Gly 200 205 210 215			679
aaa ccc aat ttg gtg gac tac ttt cct ttc ctt gag aaa att gat ccg Lys Pro Asn Leu Val Asp Tyr Phe Pro Phe Leu Glu Lys Ile Asp Pro 220 225 230			727
caa ggt ata aag cga cgc atg act aat aat ttt act aag ttt ctt ggc Gln Gly Ile Lys Arg Arg Met Thr Asn Asn Phe Thr Lys Phe Leu Gly 235 240 245			775
ctt atc agc ggt ttg att gat gac cggtt aag gaa agg aat cta agg Leu Ile Ser Gly Leu Ile Asp Asp Arg Leu Lys Glu Arg Asn Leu Arg 250 255 260			823
gac aat gca aat att gat gtt tta gac gcc ctt ctc aac att agc caa Asp Asn Ala Asn Ile Asp Val Leu Asp Ala Leu Leu Asn Ile Ser Gln 265 270 275			871
gag aac cca gaa gag att gac agg aat caa atc gag cag ttg tgt ctg Glu Asn Pro Glu Glu Ile Asp Arg Asn Gln Ile Glu Gln Leu Cys Leu 280 285 290 295			919
gac ttg ttt gca gca ggg act gat act aca tcg aat acc ttg gag tgg Asp Leu Phe Ala Ala Gly Thr Asp Thr Thr Ser Asn Thr Leu Glu Trp 300 305 310			967

gca atg gca gaa cta ctt cag aat cca cac aca ttg cag aaa gca caa Ala Met Ala Glu Leu Leu Gln Asn Pro His Thr Leu Gln Lys Ala Gln 315 320 325			1015
gaa gaa ctt gca caa gtc att ggt aaa ggc aaa caa gta gaa gaa gca Glu Glu Leu Ala Gln Val Ile Gly Lys Gly Lys Gln Val Glu Glu Ala			1063

330	335	340	
gat gtt gga cga cta cct tac ttg cga tgc ata gtg aaa gaa acc tta Asp Val Gly Arg Leu Pro Tyr Leu Arg Cys Ile Val Lys Glu Thr Leu 345 350 355			1111
cga ata cac cca gcg gct cct ctc tta att cca cgt aaa gtg gag gaa Arg Ile His Pro Ala Ala Pro Leu Leu Ile Pro Arg Lys Val Glu Glu 360 365 370 375			1159
gac gtt gag ttg tct acc tat att att cca aag gat tca caa gtt cta Asp Val Glu Leu Ser Thr Tyr Ile Ile Pro Lys Asp Ser Gln Val Leu 380 385 390			1207
gtg aac gta tgg gca att gga cgc aac tct gat cta tgg gaa aat cct Val Asn Val Trp Ala Ile Gly Arg Asn Ser Asp Leu Trp Glu Asn Pro 395 400 405			1255
ttg gtc ttt aag cca gaa agg ttt tgg gag tca gaa ata gat atc cga Leu Val Phe Lys Pro Glu Arg Phe Trp Glu Ser Glu Ile Asp Ile Arg 410 415 420			1303
ggt cga gat ttt gaa ctc att cca ttt ggt gct ggt cga aga att tgc Gly Arg Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys 425 430 435			1351
cct gga ttg cct ttg gct atg agg atg att cca gta gca cta ggt tca Pro Gly Leu Pro Leu Ala Met Arg Met Ile Pro Val Ala Leu Gly Ser 440 445 450 455			1399
ttg cta aac tca ttt aat tgg aaa cta tat ggt gga att gca cct aaa Leu Leu Asn Ser Phe Asn Trp Lys Leu Tyr Gly Gly Ile Ala Pro Lys 460 465 470			1447
gat ttg gac atg cag gaa aag ttt ggc att acc ttg gcg aaa gcc caa Asp Leu Asp Met Gln Glu Lys Phe Gly Ile Thr Leu Ala Lys Ala Gln 475 480 485			1495
cct ctg cta gct atc cca act ccc ctg tag ctataggat aaattaagtt Pro Leu Leu Ala Ile Pro Thr Pro Leu 490 495			1545
gaggttttaa gttacttagta gattcttattg cagctataagg atttcttca ccatcacgta 1605			
tgctttaccg ttggatgatg gaaaagaata tctatagctt tgggttgtt tagttgcac 1665			
ataaaaaattg aatgaatgga ataccatgga gttataagaa ataataagac tatgattctt 1725			
accctacttg aacaatgaca tggctatttc ac			
1757			

<210> 27
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 27
ttttttttt tttttta 18

<210> 28
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 28
ttttttttt ttttttc 18

<210> 29
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 29
ttttttttt ttttttg 18

<210> 30
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<400> 30
Trp Ala Ile Gly Arg Asp Pro
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<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

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<221> Modified Base
<222> (6)
<223> n is inosine - - - - -

<220>
<221> Modified Base
<222> (9)
<223> n is inosine

<220>
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<223> n is inosine

<220>
<221> Modified Base
<222> (15)
<223> n is inosine

<400> 31
tgggcnatng gnmgnaycc

20

<210> 32
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<400> 32
Phe Arg Pro Glu Arg Phe
1 5

<210> 33
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<220>
<221> Modified base
<222> (11)
<223> n is inosine

<220>
<221> Modified base
<222> (14)
<223> n is inosine

<220>
<221> Modified base
<222> (20)
<223> n is inosine

<400> 33
agaattymg nccngarmgn tt

22

<210> 34
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<220>
<221> Modified base
<222> (3)
<223> n is inosine

<220>
<221> Modified base
<222> (9)
<223> n is inosine

<220>
<221> Modified base
<222> (12)
<223> n is inosine

<220>
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<222> (15)
<223> n is inosine

<220>
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<222> (18)
<223> n is inosine

<220>
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<222> (21)
<223> n is inosine

<220>
<221> Modified base
<222> (24)
<223> n is inosine

<220>
<221> Modified base
<222> (30)
<223> n is inosine

<400> 34
ccnttyggng cnggnmgnmg natntgkscn gg

32

<210> 35
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:- Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<220>
<221> UNSURE
<222> (3)
<223> Xaa can be any amino acid.

<400> 35
Glu Phe Xaa Pro Glu Arg Phe
1 5

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<220>
<221> Modified base
<222> (3)
<223> n is inosine

<220>
<221> Modified base
<222> (7)
<223> n is inosine

<220>
<221> Modified base
<222> (8)
<223> n is inosine

<220>
<221> Modified base
<222> (9)
<223> n is inosine

<220>
<221> Modified base
<222> (12)
<223> n is inosine

<220>
<221> Modified base
<222> (15)
<223> n is inosine

<220>
<221> Modified base
<222> (18)
<223> n is inosine

<400> 36
ganttynnnnc cnganmgntt

20

<210> 37
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 37
ccacacgagt agtttggca tttgaccc

28

<210> 38
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 38
gtcttgaca tcacac ttca atctg

25

<210> 39
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 39
ccgaattccc ccccccc

17

<210> 40
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<220>
<221> Modified base
<222> (3)
<223> n is inosine

<220>
<221> Modified base
<222> (9)
<223> n is inosine

<220>
<221> Modified base
<222> (12)
<223> n is inosine

<220>
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<222> (18)
<223> n is inosine

<220>
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<222> (21)
<223> n is inosine

<220>
<221> Modified base
<222> (24)
<223> n is inosine

<220>
<221> Modified base
<222> (30)
<223> n is inosine

<400> 40
ccnggrcana tnckyytncc ngcncraan gg

32

<210> 41
<211> 496
<212> PRT
<213> Petunia sp.

<400> 41

Met Asp Tyr Val Asn Ile Leu Leu Gly Leu Phe Phe Thr Trp Phe Leu
1 5 10 15
Val Asn Gly Leu Met Ser Leu Arg Arg Arg Lys Ile Ser Lys Lys Leu
20 25 30
Pro Pro Gly Pro Phe Pro Leu Pro Ile Ile Gly Asn Leu His Leu Leu
35 40 45
Gly Asn His Pro His Lys Ser Leu Ala Gln Leu Ala Lys Ile His Gly
50 55 60
Pro Ile Met Asn Leu Lys Leu Gly Gln Leu Asn Thr Val Val Ile Ser
65 70 75 80
Ser Ser Val Val Ala Arg Glu Val Leu Gln Lys Gln Asp Leu Thr Phe
85 90 95
Ser Asn Arg Phe Val Pro Asp Val Val His Val Arg Asn His Ser Asp
100 105 110
Phe Ser Val Val Trp Leu Pro Val Asn Ser Arg Trp Lys Thr Leu Arg
115 120 125
Lys Ile Met Asn Ser Ser Ile Phe Ser Gly Asn Lys Leu Asp Gly Asn
130 135 140

Gln His Leu Arg Ser Lys Lys Val Gln Glu Leu Ile Asp Tyr Cys Gln
145 150 155 160
Lys Cys Ala Lys Asn Gly Glu Ala Val Asp Ile Gly Arg Ala Thr Phe
165 170 175
Gly Thr Thr Leu Asn Leu Leu Ser Asn Thr Ile Phe Ser Lys Asp Leu
180 185 190
Thr Asn Pro Phe Ser Asp Ser Ala Lys Glu Phe Lys Glu Leu Val Trp
195 200 205
Asn Ile Met Val Glu Ala Gly Lys Pro Asn Leu Val Asp Tyr Phe Pro
210 215 220
Phe Leu Glu Lys Ile Asp Pro Gln Gly Ile Lys Arg Arg Met Thr Asn
225 230 235 240
Asn Phe Thr Lys Phe Leu Gly Leu Ile Ser Gly Leu Ile Asp Asp Arg
245 250 255
Leu Lys Glu Arg Asn Leu Arg Asp Asn Ala Asn Ile Asp Val Leu Asp
260 265 270
Ala Leu Leu Asn Ile Ser Gln Glu Asn Pro Glu Glu Ile Asp Arg Asn
275 280 285
Gln Ile Glu Gln Leu Cys Leu Asp Leu Phe Ala Ala Gly Thr Asp Thr
290 295 300
Thr Ser Asn Thr Leu Glu Trp Ala Met Ala Glu Leu Leu Gln Asn Pro
305 310 315 320
His Thr Leu Gln Lys Ala Gln Glu Glu Leu Ala Gln Val Ile Gly Lys
325 330 335
Gly Lys Gln Val Glu Glu Ala Asp Val Gly Arg Leu Pro Tyr Leu Arg

	340	345	350
Cys Ile Val Lys Glu Thr Leu Arg Ile His Pro Ala Ala Pro Leu Leu	355	360	365
Ile Pro Arg Lys Val Glu Glu Asp Val Glu Leu Ser Thr Tyr Ile Ile	370	375	380
Pro Lys Asp Ser Gln Val Leu Val Asn Val Trp Ala Ile Gly Arg Asn	385	390	395
Ser Asp Leu Trp Glu Asn Pro Leu Val Phe Lys Pro Glu Arg Phe Trp	405	410	415
Glu Ser Glu Ile Asp Ile Arg Gly Arg Asp Phe Glu Leu Ile Pro Phe	420	425	430
Gly Ala Gly Arg Arg Ile Cys Pro Gly Leu Pro Leu Ala Met Arg Met	435	440	445
Ile Pro Val Ala Leu Gly Ser Leu Leu Asn Ser Phe Asn Trp Lys Leu	450	455	460
Tyr Gly Gly Ile Ala Pro Lys Asp Leu Asp Met Gln Glu Lys Phe Gly	465	470	475
Ile Thr Leu Ala Lys Ala Gln Pro Leu Leu Ala Ile Pro Thr Pro Leu	485	490	495

<210> 42

<211> 513

<212> PRT

<213> Arabidopsis thaliana

<400> 42

Met Ala Thr Leu Phe Leu Thr Ile Leu Leu Ala Thr Val Leu Phe Leu	1	5	10	15
-----------------------------------------------------------------	---	---	----	----

Ile Leu Arg Ile Phe Ser His Arg Arg Asn Arg Ser His Asn Asn Arg	20	25	30
-----------------------------------------------------------------	----	----	----

Leu Pro Pro Gly Pro Asn Pro Trp Pro Ile Ile Gly Asn Leu Pro His	35	40	45
-----------------------------------------------------------------	----	----	----

Met Gly Thr Lys Pro His Arg Thr Leu Ser Ala Met Val Thr Thr Tyr	50	55	60
-----------------------------------------------------------------	----	----	----

Gly Pro Ile Leu His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala	65	70	75	80
-----------------------------------------------------------------	----	----	----	----

Ala Ser Lys Ser Val Ala Glu Gln Phe Leu Lys Ile His Asp Ala Asn	85	90	95
-----------------------------------------------------------------	----	----	----

Phe Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Met Ala Tyr Asn	100	105	110
-----------------------------------------------------------------	-----	-----	-----

Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly His Arg Trp Arg Leu Leu	115	120	125
-----------------------------------------------------------------	-----	-----	-----

Arg Lys Ile Ser Ser Val His Leu Phe Ser Ala Lys Ala Leu Glu Asp	130	135	140
-----------------------------------------------------------------	-----	-----	-----

Phe Lys His Val Arg Gln Glu Glu Val Gly Thr Leu Thr Arg Glu Leu	145	150	155	160
-----------------------------------------------------------------	-----	-----	-----	-----

Val Arg Val Gly Thr Lys Pro Val Asn Leu Gly Gln Leu Val Asn Met	165	170	175
-----------------------------------------------------------------	-----	-----	-----

Cys Val Val Asn Ala Leu Gly Arg Glu Met Ile Gly Arg Arg Leu Phe

180	185	190
Gly Ala Asp Ala Asp His Lys Ala Asp Glu Phe Arg Ser Met Val Thr		
195	200	205
Glu Met Met Ala Leu Ala Gly Val Phe Asn Ile Gly Asp Phe Val Pro		
210	215	220
Ser Leu Asp Trp Leu Asp Leu Gln Gly Val Ala Gly Lys Met Lys Arg		
225	230	235
Leu His Lys Arg Phe Asp Ala Phe Leu Ser Ser Ile Leu Lys Glu His		
245	250	255
Glu Met Asn Gly Gln Asp Gln Lys His Thr Asp Met Leu Ser Thr Leu		
260	265	270
Ile Ser Leu Lys Gly Thr Asp Leu Asp Gly Asp Gly Ser Leu Thr		
275	280	285
Asp Thr Glu Ile Lys Ala Leu Leu Asn Met Phe Thr Ala Gly Thr		
290	295	300
Asp Thr Ser Ala Ser Thr Val Asp Trp Ala Ile Ala Glu Leu Ile Arg		
305	310	315
His Pro Asp Ile Met Val Lys Ala Gln Glu Glu Leu Asp Ile Val Val		
325	330	335
Gly Arg Asp Arg Pro Val Asn Glu Ser Asp Ile Ala Gln Leu Pro Tyr		
340	345	350
Leu Gln Ala Val Ile Lys Glu Asn Phe Arg Leu His Pro Pro Thr Pro		
355	360	365
Leu Ser Leu Pro His Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr		
370	375	380
His Ile Pro Lys Gly Ser Thr Leu Leu Thr Asn Ile Trp Ala Ile Ala		
385	390	395
Arg Asp Pro Asp Gln Trp Ser Asp Pro Leu Ala Phe Lys Pro Glu Arg		
405	410	415
Phe Leu Pro Gly Gly Glu Lys Ser Gly Val Asp Val Lys Gly Ser Asp		
420	425	430
Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu		
435	440	445
Ser Leu Gly Leu Arg Thr Ile Gln Phe Leu Thr Ala Thr Leu Val Gln		
450	455	460
Gly Phe Asp Trp Glu Leu Ala Gly Gly Val Thr Pro Glu Lys Leu Asn		
465	470	475
Met Glu Glu Ser Tyr Gly Leu Thr Leu Gln Arg Ala Val Pro Leu Val		
485	490	495

Val His Pro Lys Pro Arg Leu Ala Pro Asn Val Tyr Gly Leu Gly Ser
500 505 510

Gly

<210> 43
<211> 7
<212> PRT
<213> Arabidopsis thaliana

<400> 43
Arg Pro Pro Asn Ser Gly Ala
1 5

<210> 44
<211> 17
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (8)
<223> Xaa can be any amino acid.

<220>
<221> UNSURE
<222> (10)
<223> Xaa cab be any amino acid.

<220>
<221> UNSURE
<222> (15)
<223> Xaa can be any amino acid.

<400> 44
Arg Pro Pro Asn Ser Gly Ala Xaa His Xaa Ala Tyr Asn Tyr Xaa Asp
1 5 10 15

Leu

<210> 45
<211> 521
<212> PRT
<213> Arabidopsis thaliana

<220>
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<222> (8)
<223> Xaa can be any amino acid.

<220>
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<222> (10)
<223> Xaa cab be any amino acid.

<220>

<221> UNSURE

<222> (15)

<223> Xaa can be any amino acid.

<220>

<221> UNSURE

<222> (18)...(517)

<223> Xaa can be any amino acid. Positions 18-517
can be 0-500 amino acids.

<400> 45

Arg Pro Pro Asn Ser Gly Ala Xaa His Xaa Ala Tyr Asn Tyr Xaa Asp
1 5 10 15

Leu Xaa
20 25 30

Xaa
35 40 45

Xaa
50 55 60

Xaa
65 70 75 80

Xaa
.85 90 95

Xaa
100 105 110

Xaa
115 120 125

Xaa
130 135 140

Xaa
145 150 155 160

Xaa
165 170 175

Xaa
180 185 190

Xaa
195 200 205

Xaa
210 215 220

Xaa
225 230 235 240

Xaa
245 250 255

Xaa
260 265 270

Xaa
275 280 285

Xaa
290 295 300

Xaa
305 310 315 320

Xaa
325 330 335

Xaa
340 345 350

Xaa
355 360 365

Xaa
370 375 380

Xaa
385 390 395 400

Xaa
405 410 415

Xaa
420 425 430

Xaa
435 440 445

Xaa
450 455 460

Xaa
465 470 475 480

Xaa
485 490 495

Xaa
500 505 510

Xaa Xaa Xaa Xaa Gly Gly Glu Lys
515 520